



IFWO

RAW SEQUENCE LISTING

DATE: 08/04/2004

PATENT APPLICATION: US/10/782,234

TIME: 10:45:29

Input Set : N:\CrF3\RULE60\10782234.raw

Output Set: N:\CRF4\08042004\J782234.raw

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1 <110> APPLICANT: Burian, Jan
2     Kuzyk, Michael
3     Thornton, Julian
4     Kay, William
5 <120> TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
6     RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
7 <130> FILE REFERENCE: IDC01/60485/US
8 <140> CURRENT APPLICATION NUMBER: US/10/782,234
9 <141> CURRENT FILING DATE: 2004-02-18
10 <150> PRIOR APPLICATION NUMBER: US/09/677,374
11 <151> PRIOR FILING DATE: 2000-09-15
12 <150> PRIOR APPLICATION NUMBER: US 60/154,437
13 <151> PRIOR FILING DATE: 1999-09-17
14 <150> PRIOR APPLICATION NUMBER: NO 20004637
15 <151> PRIOR FILING DATE: 2000-09-15
16 <150> PRIOR APPLICATION NUMBER: IE 2000/0752
17 <151> PRIOR FILING DATE: 2000-09-18
18 <150> PRIOR APPLICATION NUMBER: GB 0022825.4
19 <151> PRIOR FILING DATE: 2000-09-18
20 <150> PRIOR APPLICATION NUMBER: CL 2544-2000
21 <151> PRIOR FILING DATE: 2000-09-15
22 <160> NUMBER OF SEQ ID NOS: 20
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 486
27 <212> TYPE: DNA
28 <213> ORGANISM: Piscirickettsia salmonis
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(486)
32 <400> SEQUENCE: 1
33     atg aac aga gga tgt ttg caa ggt agt agt cta att att atc agt gtg 48
34     Met Asn Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val
35     1             5             10             15
36     ttt tta gtt ggc tgt gcc cag aac ttt agt cgt caa gaa gtc gga gct 96
37     Phe Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala
38     20             25             30
39     gcg act ggg gct gtt gtt ggc ggt gtt gct ggc cag ctg ttt ggt aaa 144
40     Ala Thr Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys
41     35             40             45
42     ggt agt ggt cga gtt gca atg gcc att ggt ggt gct gtt ttg ggt gga 192
43     Gly Ser Gly Arg Val Ala Met Ala Ile Gly Gly Ala Val Leu Gly Gly
44     50             55             60

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45   tta att ggt tct aaa atc ggt caa tcg atg gat cag cag gat aaa ata 240
46   Leu Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile
47   65                               70                               75                               80
48   aag cta aac cag agt ttg gaa aag gta aaa gca ggg caa gtg aca cgt 288
49   Lys Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg
50   85                               90                               95
51   tgg cgt aat cca gat aca ggc aat agt tat agt gtt gag cca gtg cgt 336
52   Trp Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg
53   100                             105                             110
54   act tac cag cgt tac aat aag caa gag cgt cgc cag caa tat tgt cga 384
55   Thr Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg
56   115                             120                             125
57   gaa ttt cag caa aag gcg atg att gca ggg cag aag caa gag att tac 432
58   Glu Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr
59   130                             135                             140
60   ggc act gca tgc cgg caa ccg gat ggt cgt tgg caa gtc att tca aca 480
61   Gly Thr Ala Cys Arg Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr
62   145                             150                             155                             160
63   gaa aaa                                                                486
64   Glu Lys
66 <210> SEQ ID NO: 2
67 <211> LENGTH: 162
68 <212> TYPE: PRT
69 <213> ORGANISM: Piscirickettsia salmonis
70 <400> SEQUENCE: 2
71   Met Asn Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val
72   1                               5                               10                               15
73   Phe Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala
74   20                             25                             30
75   Ala Thr Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys
76   35                             40                             45
77   Gly Ser Gly Arg Val Ala Met Ala Ile Gly Gly Ala Val Leu Gly Gly
78   50                             55                             60
79   Leu Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile
80   65                             70                             75                             80
81   Lys Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg
82   85                             90                             95
83   Trp Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg
84   100                           105                           110
85   Thr Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg
86   115                           120                           125
87   Glu Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr
88   130                           135                           140
89   Gly Thr Ala Cys Arg Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr
90   145                           150                           155                           160
91   Glu Lys
93 <210> SEQ ID NO: 3
94 <211> LENGTH: 483
95 <212> TYPE: DNA

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96 <213> ORGANISM: Piscirickettsia salmonis
97 <220> FEATURE:
98 <221> NAME/KEY: CDS
99 <222> LOCATION: (1)..(483)
100 <400> SEQUENCE: 3
101   atg cgt ggt tgc ctg cag ggc agc tct ctg atc att atc tct gtt ttc 48
102   Met Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val Phe
103   1           5           10           15
104   ctg gtg ggt tgc gcc cag aac ttc agc cgc cag gaa gtt ggc gcg gcc 96
105   Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala
106   20           25           30
107   acc ggt gcg gtt gtg ggc ggt gtt gcc ggc cag ctg ttc ggt aaa ggc 144
108   Thr Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys Gly
109   35           40           45
110   tct ggt cgt gtg tgc atg gcc atc ggc ggt gcg gtt ctg ggc ggt ctg 192
111   Ser Gly Arg Val Ser Met Ala Ile Gly Gly Ala Val Leu Gly Gly Leu
112   50           55           60
113   att ggc tct aaa atc ggt cag agc atg gac cag cag gat aaa atc aaa 240
114   Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile Lys
115   65           70           75           80
116   ctg aac cag tct ctg gaa aaa gtg aaa gcc ggc cag gtt act cgt tgg 288
117   Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg Trp
118   85           90           95
119   cgt aat ccg gac acc ggt aac agc tac tct gtg gaa ccg gtt cgc acc 336
120   Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg Thr
121   100          105          110
122   tac cag cgt tac aac aaa cag gaa cgc cgt cag cag tac tgc cgc gaa 384
123   Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg Glu
124   115          120          125
125   ttt cag cag aaa gcc atg atc gca ggt cag aaa cag gaa atc tac ggc 432
126   Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr Gly
127   130          135          140
128   acc gcg tgc cct cag ccg gat ggc cgc tgg cag gtg att agc acc gaa 480
129   Thr Ala Cys Pro Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr Glu
130   145          150          155          160
131   aaa
132   Lys
133   483
134 <210> SEQ ID NO: 4
135 <211> LENGTH: 161
136 <212> TYPE: PRT
137 <213> ORGANISM: Piscirickettsia salmonis
138 <400> SEQUENCE: 4
139   Met Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val Phe
140   1           5           10           15
141   Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala
142   20           25           30
143   Thr Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys Gly
144   35           40           45
145   Ser Gly Arg Val Ser Met Ala Ile Gly Gly Ala Val Leu Gly Gly Leu

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146          50          55          60
147   Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile Lys
148   65          70          75          80
149   Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg Trp
150          85          90          95
151   Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg Thr
152          100          105          110
153   Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg Glu
154          115          120          125
155   Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr Gly
156          130          135          140
157   Thr Ala Cys Pro Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr Glu
158          145          150          155          160
159   Lys

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161 <210> SEQ ID NO: 5

162 <211> LENGTH: 768

163 <212> TYPE: DNA

164 <213> ORGANISM: *Piscirickettsia salmonis*

165 <220> FEATURE:

166 <221> NAME/KEY: CDS

167 <222> LOCATION: (1)..(768)

168 <221> NAME/KEY: sig_peptide

169 <222> LOCATION: (1)..(285)

W--> 170 <221> mat_peptide

171 <222> LOCATION: (286)..(768)

W--> 172 <400> 5

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175   -95          -90          -85          -80
176   att aca cca ata atc aaa att act aac aca tct gac agt gat tta aat 96
177   Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
178          -75          -70          -65
179   tta aat gac gta aaa gtt aga tat tat tac aca agt gat ggt aca caa 144
180   Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
181          -60          -55          -50
182   gga caa act ttc tgg tgt gac cat gct ggt gca tta tta gga aat agc 192
183   Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
184          -45          -40          -35
185   tat gtt gat aac act agc aaa gtg aca gca aac ttc gtt aaa gaa aca 240
186   Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
187          -30          -25          -20
188   gca agc cca aca tca acc tat gat aca tat ctg gat ccg tct cat atg 288
189   Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Leu Asp Pro Ser His Met
190          -15          -10          -5          1
191   cgt ggt tgc ctg cag ggc agc tct ctg atc att atc tct gtt ttc ctg 336
192   Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val Phe Leu
193          5          10          15
194   gtg ggt tgc gcc cag aac ttc agc cgc cag gaa gtt ggc gcg gcc acc 384
195   Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala Thr

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196          20          25          30
197      ggt gcg gtt gtg ggc ggt gtt gcc ggc cag ctg ttc ggt aaa ggc tct 432
198      Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys Gly Ser
199          35          40          45
200      ggt cgt gtg tct atg gcc atc ggc ggt gcg gtt ctg ggc ggt ctg att 480
201      Gly Arg Val Ser Met Ala Ile Gly Gly Ala Val Leu Gly Gly Leu Ile
202      50          55          60          65
203      ggc tct aaa atc ggt cag agc atg gac cag cag gat aaa atc aaa ctg 528
204      Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile Lys Leu
205          70          75          80
206      aac cag tct ctg gaa aaa gtg aaa gcc ggc cag gtt act cgt tgg cgt 576
207      Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg Trp Arg
208          85          90          95
209      aat ccg gac acc ggt aac agc tac tct gtg gaa ccg gtt cgc acc tac 624
210      Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg Thr Tyr
211          100          105          110
212      cag cgt tac aac aaa cag gaa cgc cgt cag cag tac tgc cgc gaa ttt 672
213      Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg Glu Phe
214          115          120          125
215      cag cag aaa gcc atg atc gca ggt cag aaa cag gaa atc tac ggc acc 720
216      Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr Gly Thr
217      130          135          140          145
218      gcg tgc cct cag ccg gat ggc cgc tgg cag gtg att agc acc gaa aaa 768
219      Ala Cys Pro Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr Glu Lys
220          150          155          160
222 <210> SEQ ID NO: 6
223 <211> LENGTH: 256
224 <212> TYPE: PRT
225 <213> ORGANISM: Piscirickettsia salmonis
226 <220> FEATURE:
227 <221> NAME/KEY: SIGNAL
228 <222> LOCATION: (-95)..(-1)
229 <400> SEQUENCE: 6
230      Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
231      -95          -90          -85          -80
232      Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
233          -75          -70          -65
234      Leu Asn Asp Val Lys Val Arg Tyr Tyr Thr Ser Asp Gly Thr Gln
235          -60          -55          -50
236      Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
237          -45          -40          -35
238      Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
239          -30          -25          -20
240      Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Leu Asp Pro Ser His Met
241      -15          -10          -5          1
242      Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val Phe Leu
243          5          10          15
244      Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala Thr
245          20          25          30

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VERIFICATION SUMMARY

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Input Set : **N:\Crf3\RULE60\10782234.raw**

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L:374 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
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